GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2003, 19:55:10 ; Search time 255 Seconds
(without alignments)
3705.111 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 350
Sequence: 1 MDLKALLSSLNDFASLSFAE.....LENKINIILSETDRDPLQVV 350

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103490

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=p2noli.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09745506_@CGN_1_1_0_@runat_22082003_104427_7254 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	350	100.0	1053	22	AAH52212	Human AFP protein
	2	350	100.0	1574	22	AAH16397	Human cDNA sequenc
	3	350	100.0	1696	22	AAK60866	Human immune/haema
	4	350	100.0	1739	23	ABV23243	Human prostate exp
	5	350	100.0	1739	23	ABV29087	Human prostate exp
	6	311	88.9	1398	22	AAF59945	Human gene express
	7	296	84.6	1554	22	AAS44644	Human full-length
	8	211	60.3	1385	24	ABL60919	Human protein kina
c	9	155	44.3	1686	23	AAS85172	DNA encoding novel
	10	122	34.9	462	22	AAL23953	Human breast cance
	11	122	34.9	796	22	AAH07192	Human cDNA clone (
	12	119	34.0	14969	22	AAK78763	Human immune/haema
	13	90	25.7	514	22	AAL15105	Human breast cance
c	14	73	20.9	465	22	ABA46423	Human breast cell
c	15	73	20.9	465	22	ABA57019	Human foetal liver
c	16	73	20.9	465	22	AAK05073	Human brain expres
c	17	73	20.9	465	22	AAI15235	Probe #5168 for ge
c	18	73	20.9	465	22	AAI04973	Probe #4964 used t
c	19	73	20.9	465	23	ABS30297	Human liver single
	20	70	20.0	249	21	AAC25260	Human secreted pro
c	21	69	19.7	208	22	ABA51524	Human breast cell
c	22	69	19.7	208	22	ABA69581	Human foetal liver
c	23	69	19.7	208	22	AAK17792	Human brain expres
c	24	69	19.7	208	22	AAI24414	Probe #14347 for g
c	25	69	19.7	208	22	AAI09950	Probe #9941 used t
c	26	69	19.7	208	23	ABS43283	Human liver single
	27	53	15.1	394	25	ABX45683	Bovine EST associa
	28	49	14.0	633	22	AAS34287	Human cDNA encodin
	29	43	12.3	513	22	AAS44816	Human contig polyn
	30	38	10.9	495	23	AAS85169	DNA encoding novel
	31	25	7.1	522	23	AAS85171	DNA encoding novel
	32	19	5.4	60	24	ABN33267	Human spliced tran
	33	19	5.4	273	23	ABV35380	Human prostate exp
	34	19	5.4	273	23	ABV44212	Human prostate exp
	35	19	5.4	443	23	ABV14293	Human prostate exp
	36	18	5.1	357	23	ABV05124	Human prostate exp
	37	13	3.7	41	24	ABL60924	Human protein kina
	38	10	2.9	339	21	AAC17249	Human secreted pro
c	39	10	2.9	400	18	AAV75090	Staphylococcus aur
	40	10	2.9	463	22	AAK63571	Human immune/haema
	41	10	2.9	1083	22	AAH53378	S. epidermidis ope
	42	10	2.9	1104	24	ABN91378	Staphylococcus epi
	43	10	2.9	3041	22	AAH55004	S. epidermidis gen
	44	10	2.9	3138	22	AAH54589	S. epidermidis gen
	45	10	2.9	3441	22	AAH54443	S. epidermidis gen

ALIGNMENTS

RESULT 1
AAH52212
ID AAH52212 standard; cDNA; 1053 BP.
XX
AC AAH52212;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human AFP protein encoding cDNA sequence SEQ ID NO:239.
XX
KW Human; secreted protein; secretion; bacterial cell; fungal cell;
KW eukaryotic cell; fusion protein; maltose binding protein;
KW immunoglobulin constant region; polyhistidine tag; ss.
XX
OS Homo sapiens.
XX
PN WO200129221-A2.

```
XX
PD   26-APR-2001.
XX
PF   20-OCT-2000; 2000WO-US29052.
XX
PR   20-OCT-1999;   99US-0160712.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Conklin DC,  Yee DP;
XX
DR   WPI; 2001-300340/31.
DR   P-PSDB; AAG81361.
XX
PT   Isolated polypeptide for directing secretion of proteins of interest
PT   from a host cell including, e.g. bacteria, includes contiguous amino
PT   acid residues of polypeptide with specified amino acids  -
XX
PS   Claim 9; Page 422-424; 617pp; English.
XX
CC   AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242
CC   to AAG81453. The secreted proteins can be used for directing the
CC   secretion of proteins of interest from a host cell including bacteria,
CC   fungal cells, and cultured higher eukaryotic cells. The present invention
CC   also describes fusion proteins, where a secreted protein of the invention
CC   is operably linked via a peptide bond or peptide linker to a second
CC   protein selected from the group consisting of maltose binding protein,
CC   an immunoglobulin constant region, a polyhistidine tag and a peptide
CC   given in AAG81453.
XX
SQ   Sequence 1053 BP; 279 A; 253 C; 247 G; 274 T; 0 other;

Alignment Scores:
Pred. No.:              0           Length:         1053
Score:                  350.00      Matches:        350
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            100.00%     Indels:         0
DB:                     22          Gaps:           0

US-09-745-506-37 (1-350) x AAH52212 (1-1053)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
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Db          1 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 60

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 120

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 180

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 240

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 300

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 360

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 420

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
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Db        421 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 480

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
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Db        481 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 540

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
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Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
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Db        601 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 660

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
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Db        661 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 720

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
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Db        721 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 780

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
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Db        781 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 840

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
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Db        841 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 900

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
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Db        901 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 960

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
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Db        961 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1020

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
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Db       1021 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1050

RESULT 2
AAH16397
ID   AAH16397 standard; cDNA; 1574 BP.
XX
AC   AAH16397;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:15359.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
```

```
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 15359; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 1574 BP; 420 A; 361 C; 372 G; 421 T; 0 other;

Alignment Scores:
Pred. No.:                0          Length:          1574
Score:                    350.00     Matches:         350
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              100.00%    Indels:          0
DB:                       22         Gaps:            0

US-09-745-506-37 (1-350) x AAH16397 (1-1574)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
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Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 390

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 450

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 510

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 570

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 630

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 690

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
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Db        691 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 750

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 810

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 870

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 930

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 990

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1050

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1110

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
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Db       1111 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1170

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
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Db       1171 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1230

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
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Db       1231 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1290

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              |||||||||||||||||||||||||||||
Db       1291 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1320

RESULT 3
AAK60866
ID   AAK60866 standard; cDNA; 1696 BP.
XX
AC   AAK60866;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:5926.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
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PR 30-JUN-2000; 2000US-0215135.
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PR 08-DEC-2000; 2000US-0251868.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR P-PSDB; AAM88085.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Claim 1; SEQ ID NO 5926; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased

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CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 1696 BP; 510 A; 369 C; 379 G; 435 T; 3 other;

Alignment Scores:
Pred. No.:              0           Length:         1696
Score:                  350.00      Matches:        350
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            100.00%     Indels:         0
DB:                     22          Gaps:           0

US-09-745-506-37 (1-350) x AAK60866 (1-1696)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 366

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 426

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 486

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 546

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 606

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 666

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 726

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 786

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 846

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 906

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 966

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 1026

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1086

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1146

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1206

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1266

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1326

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              ||||||||||||||||||||||||||||||
Db       1327 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1356

RESULT 4
ABV23243
ID   ABV23243 standard; cDNA; 1739 BP.
XX
AC   ABV23243;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 23234.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 4189-4190; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
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CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 1739 BP; 457 A; 389 C; 411 G; 473 T; 9 other;

Alignment Scores:
Pred. No.:              0              Length:          1739
Score:                  350.00         Matches:         350
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     23             Gaps:            0

US-09-745-506-37 (1-350) x ABV23243 (1-1739)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 356

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 416

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 476

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 536

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 596

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 656

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 716

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 776

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 836

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 896

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 956

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 1016

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1076

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1136

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1196

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1256

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1316

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              |||||||||||||||||||||||||||||||
Db       1317 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1346

RESULT 5
ABV29087
ID   ABV29087 standard; cDNA; 1739 BP.
XX
AC   ABV29087;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 29078.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 6170; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
```

```
SQ   Sequence 1739 BP; 457 A; 389 C; 411 G; 473 T; 9 other;

Alignment Scores:
Pred. No.:              0              Length:          1739
Score:                  350.00         Matches:         350
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     23             Gaps:            0

US-09-745-506-37 (1-350) x ABV29087 (1-1739)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 356

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 416

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 476

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 536

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 596

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 656

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 716

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 776

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 836

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 896

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 956

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 1016

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1076

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1136

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1196

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1256

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1316

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              |||||||||||||||||||||||||||||
Db       1317 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1346

RESULT 6
AAF59945
ID   AAF59945 standard; cDNA; 1398 BP.
XX
AC   AAF59945;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human gene expression regulatory factor-related protein hNIF3-s cDNA.
XX
KW   Human gene expression regulatory factor-related protein; hNIF3-s;
KW   NGG1-interacting factor; haemopoietic stem cell; preparation;
KW   detection; ss.
XX
OS   Homo sapiens.
XX
PN   CN1272543-A.
XX
PD   08-NOV-2000.
XX
PF   11-APR-2000; 2000CN-0115369.
XX
PR   11-APR-2000; 2000CN-0115369.
XX
PA   (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI   Li N,  Xiao H,  Liu F;
XX
DR   WPI; 2001-183596/19.
DR   P-PSDB; AAB60663.
XX
PT   Human gene expression regulatory factor related protein and its coded
PT   sequence -
XX
PS   Claim 1; Page 18-19; 20pp; Chinese.
XX
CC   The invention relates to a novel human gene expression regulatory
CC   factor-related protein, hNIF3-s (NGG1-interacting factor, AAB60663),
CC   and cDNA encoding it (AAF59945). hNIF3-s is expressed in haemopoietic
CC   stem cells. The invention also relates to the preparation of hNIF3-s
CC   proteins and nucleic acids, and the detection of hNIF3-s proteins and
CC   nucleic acids in a sample. The present sequence represents cDNA encoding
CC   hNIF3-s.
XX
SQ   Sequence 1398 BP; 365 A; 331 C; 342 G; 360 T; 0 other;

Alignment Scores:
Pred. No.:              1.43e-305      Length:          1398
Score:                  311.00         Matches:         350
Percent Similarity:     99.15%         Conservative:    0
Best Local Similarity:  99.15%         Mismatches:      0
Query Match:            88.86%         Indels:          3
DB:                     22             Gaps:            0

US-09-745-506-37 (1-350) x AAF59945 (1-1398)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 295

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        296 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 355

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 415

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIle-ThrTrpAsnTh 80
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        416 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATTAACCTGGAACAC 475

Qy         80 rTrp-Lys-GluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerPro 99
              |||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 ATGGGAAGGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCT 535

Qy        100 HisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CATACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGA 595

Qy        120 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsn 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAAC 655

Qy        140 HisArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaVal 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTG 715

Qy        160 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGln 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 AAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAA 775

Qy        180 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 ACACGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCC 835

Qy        200 ArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeu 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 CGGAACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTA 895

Qy        220 HisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIle 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CATACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATT 955

Qy        240 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGA 1015

Qy        260 ThrLeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeu 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 ACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTG 1075

Qy        280 GlnGlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAsp 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 CAGGGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGAT 1135

Qy        300 AlaAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPhe 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GCTGCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTT 1195

Qy        320 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 CTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTA 1255

Qy        340 SerGluThrAspArgAspProLeuGlnValVal 350
              ||||||||||||||||||||||||||||||||
Db       1256 TCAGAGACTGACAGGGACCCTCTTCAGGTGGTA 1288

RESULT 7
AAS44644
ID   AAS44644 standard; DNA; 1554 BP.
XX
AC   AAS44644;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human full-length polynucleotide sequence #69.
XX
KW   Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW   mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW   cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW   nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW   angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW   genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW   cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory;
KW   antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW   neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
KW   immunostimulant; analgesic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200164834-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04926.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
PR   17-JUN-2000; 2000US-0597707.
PR   14-JUL-2000; 2000US-0616807.
PR   19-SEP-2000; 2000US-0664641.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Asundi V,  Zhang J,  Zhao QA,  Ren F;
PI   Xue AJ,  Yang Y,  Wehrman T,  Wang J,  Ma Y,  Wang D,  Chen R,  Xu C;
PI   Drmanac R;
XX
DR   WPI; 2001-589862/66.
DR   P-PSDB; AAU27744.
XX
PT   Novel polypeptides and nucleic acids obtained from cDNA libraries
PT   prepared from various human tissues, for diagnosis, treatment of
PT   cancer, neurological, inflammatory disorders and for use in arrays for
PT   detection -
XX
PS   Claim 1; SEQ ID No 69; 153pp; English.
XX
CC   Sequences AAS44576-AAS44919 represent full-length polynucleotides and
CC   contig polynucleotides encoding polypeptides of the invention. The DNA
CC   and protein sequences are useful for the treatment, diagnosis and
CC   prevention of various types of disorder in a mammalian subject such as a
CC   human, dog, monkey, mouse, hamster or rat. The disorders include cancers
CC   such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
CC   as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC   diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC   disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC   chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC   Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC   disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC   bowel disease. The sequences exhibit activity relating to angiogenesis,
CC   cell proliferation, cell differentiation, stem cell growth factor,
CC   activin or inhibin. Therefore, they can be used to manipulate stem cells
CC   in culture to give rise to neuroepithelial cells that can be used to
CC   augment or replace cells damaged by illness, accidental damage or genetic
CC   disorders. The sequences may also be used for regeneration of bone,
CC   cartilage, tendons and ligaments and in tissue repair and burn healing.
CC   Note: Some sequences for this patent did not form part of the printed
CC   specification, but were obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1554 BP; 428 A; 358 C; 346 G; 422 T; 0 other;

Alignment Scores:
Pred. No.:              2.67e-290       Length:         1554
Score:                  296.00          Matches:        349
Percent Similarity:     99.43%          Conservative:   0
```

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Best Local Similarity:  99.43%          Mismatches:    1
Query Match:            84.57%          Indels:        2
DB:                     22              Gaps:          0

US-09-745-506-37 (1-350) x AAS44644 (1-1554)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 295

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 355

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 415

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 475

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 535

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 ACAGCCTATGATGCTGCGCCCCCAGGGCGTCAACAACTGGTTGGCTAAAGCGCTTGGAGCT 595

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 655

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 715

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 775

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 835

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 895

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 955

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1015

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1075

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThr-LeuAspAl 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db       1076 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATAT-TTTGGATGC 1134

Qy        300 aAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1135 TGCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCT 1194

Qy        320 uSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSe 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 TTCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATC 1254

Qy        340 rGluThrAspArgAspProLeuGlnValVal 350
              ||||||||||||||||||||||||||||||
Db       1255 AGAGACTGACAGGGACCCTCTTCAGGTGGTA 1285

RESULT 8
ABL60919
ID   ABL60919 standard; cDNA; 1385 BP.
XX
AC   ABL60919;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human protein kinase C 27.17 polypeptide encoding cDNA.
XX
KW   Human; protein kinase C 27.17; protein metabolism; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             389..1132
FT                   /*tag= a
FT                   /product= "protein kinase C 27.17 polypeptide"
XX
PN   CN1333355-A.
XX
PD   30-JAN-2002.
XX
PF   07-JUL-2000; 2000CN-0117049.
XX
PR   07-JUL-2000; 2000CN-0117049.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305609/35.
DR   P-PSDB; ABB08182.
XX
PT   Human protein kinase C 27.17 polypeptide and its encoding
PT   polynucleotide, for treating e.g. protein metabolism disturbance -
XX
PS   Claim 6; Page 25-26 (disclosure); 33pp; Chinese.
XX
CC   The invention relates to a human protein kinase C 27.17 polypeptide and
CC   its encoding polynucleotide. The polypeptide can be expressed by standard
CC   DNA recombination. The polynucleotide, polypeptide and its antagonist are
CC   useful for treating e.g. protein metabolism disturbance. The present
CC   sequence represents the human protein kinase C 27.17 polypeptide encoding
CC   cDNA.
XX
SQ   Sequence 1385 BP; 375 A; 324 C; 308 G; 378 T; 0 other;

Alignment Scores:
Pred. No.:              4.5e-204        Length:         1385
Score:                  211.00          Matches:        346
Percent Similarity:     98.02%          Conservative:   0
Best Local Similarity:  98.02%          Mismatches:     4
Query Match:            60.29%          Indels:         7
DB:                     24              Gaps:           0

US-09-745-506-37 (1-350) x ABL60919 (1-1385)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 141

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 201

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        202 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 261

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 321

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 381

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 441

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyr--ProThrGluGlyAsn- 139
              ||||||||||||  ||||||||||||  |||||||||  |||||||||  |||
Db        442 TGTACCTCCAGGCC-ATACATCCTTCCAA-GCTCCCAACTT-CCCCTACAGAGG--AACC 496

Qy        140 HisArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaVal 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTG 556

Qy        160 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGln 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 AAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAA 616

Qy        180 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 ACACGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCC 676

Qy        200 ArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeu 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CGGAACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTA 736

Qy        220 HisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIle 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 CATACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATT 796

Qy        240 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGA 856

Qy        260 ThrLeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeu 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTG 916

Qy        280 GlnGlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAsp 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 CAGGGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGAT 976

Qy        300 AlaAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPhe 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GCTGCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTT 1036

Qy        320 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 CTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTA 1096

Qy        340 SerGluThrAspArgAspProLeuGlnValVal 350
              ||||||||||||||||||||||||||||||||
Db       1097 TCAGAGACTGACAGGGACCCTCTTCAGGTGGTA 1129

RESULT 9
AAS85172/c
ID   AAS85172 standard; cDNA; 1686 BP.
XX
AC   AAS85172;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #20976.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG20985.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 20976; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1686 BP; 445 A; 397 C; 391 G; 452 T; 1 other;

Alignment Scores:
Pred. No.:              3.78e-147       Length:         1686
Score:                  155.00          Matches:        194
Percent Similarity:     98.48%          Conservative:   0
Best Local Similarity:  98.48%          Mismatches:     0
Query Match:            44.29%          Indels:         3
DB:                     23              Gaps:           0

US-09-745-506-37 (1-350) x AAS85172 (1-1686)

Qy         82 LysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThr 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 AAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACA 1056

Qy        102 AlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCys 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 GCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCTTGT 996

Qy        122 ThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArg 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 ACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCACCGA 936
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Qy        142 ValGluPheAsnValAsnTyrThrGlnAspLeu-AspLysValMetSer-AlaValLysG 161
              ||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Db        935 GTAGAATTCAACGTTAACTACACCCAAGACCTGGGACAAAGTCATGTCTGGCAGTGAAAG 876

Qy        161 lyIle-AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 GAATTTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 816

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 756

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 696

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 636

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 576

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGly 275
              |||||||||||||||||||||||||||||||||||||||||||||
Db        575 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGG 531
```

RESULT 10
AAL23953
ID AAL23953 standard; cDNA; 462 BP.
XX
AC AAL23953;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 16410.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1; Page 3004; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 462 BP; 103 A; 126 C; 118 G; 115 T; 0 other;

Alignment Scores:

Pred. No.:	3.34e-114	Length:	462
Score:	122.00	Matches:	122
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.86%	Indels:	0
DB:	22	Gaps:	0

US-09-745-506-37 (1-350) x AAL23953 (1-462)

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Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 155

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 215

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 275

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 335

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 395

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ACAGCCTATGATGCTGCGCCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 455

Qy        121 CysThr 122
              ||||||
Db        456 TGTACC 461
```

RESULT 11
AAH07192
ID AAH07192 standard; cDNA; 796 BP.
XX
AC AAH07192;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:4027.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

```
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 1; SEQ ID 4027; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 796 BP; 192 A; 204 C; 202 G; 195 T; 3 other;

Alignment Scores:
Pred. No.:              5.68e-114       Length:         796
Score:                  122.00          Matches:        122
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            34.86%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-37 (1-350) x AAH07192 (1-796)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 330

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 390

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 450

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 510

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 570

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ACAGCCTATGATGCTGCGCCCCAAGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 630

Qy        121 CysThr 122
              ||||||
Db        631 TGTACC 636
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RESULT 12
AAK78763
ID   AAK78763 standard; DNA; 14969 BP.
XX
AC   AAK78763;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33575.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
PR   14-AUG-2000; 2000US-0225213.
PR   14-AUG-2000; 2000US-0225214.
PR   14-AUG-2000; 2000US-0225266.
PR   14-AUG-2000; 2000US-0225267.
PR   14-AUG-2000; 2000US-0225268.
PR   14-AUG-2000; 2000US-0225270.
PR   14-AUG-2000; 2000US-0225447.
PR   14-AUG-2000; 2000US-0225757.
PR   14-AUG-2000; 2000US-0225758.
PR   14-AUG-2000; 2000US-0225759.
PR   18-AUG-2000; 2000US-0226279.
PR   22-AUG-2000; 2000US-0226681.
PR   22-AUG-2000; 2000US-0226868.
PR   22-AUG-2000; 2000US-0227182.
PR   23-AUG-2000; 2000US-0227009.
PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
PR   01-SEP-2000; 2000US-0229344.
PR   01-SEP-2000; 2000US-0229345.
PR   05-SEP-2000; 2000US-0229509.
PR   05-SEP-2000; 2000US-0229513.
PR   06-SEP-2000; 2000US-0230437.
PR   06-SEP-2000; 2000US-0230438.
PR   08-SEP-2000; 2000US-0231242.
PR   08-SEP-2000; 2000US-0231243.
PR   08-SEP-2000; 2000US-0231244.
PR   08-SEP-2000; 2000US-0231413.
PR   08-SEP-2000; 2000US-0231414.
PR   08-SEP-2000; 2000US-0232080.
PR   08-SEP-2000; 2000US-0232081.
PR   12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 33575; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 14969 BP; 4016 A; 3069 C; 3042 G; 4842 T; 0 other;

Alignment Scores:

Pred. No.:	1.11e-109	Length:	14969
Score:	119.00	Matches:	119
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.00%	Indels:	0
DB:	22	Gaps:	0

US-09-745-506-37 (1-350) x AAK78763 (1-14969)

```
Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2604 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 2663

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2664 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 2723

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2724 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 2783

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2784 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 2843

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2844 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 2903
```

```
Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2904 ACAGCCTATGATGCTGCGCCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGT 2960

RESULT 13
AAL15105
ID   AAL15105 standard; cDNA; 514 BP.
XX
AC   AAL15105;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 7562.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US00798.
XX
PR   14-JAN-2000; 2000US-0176077.
PR   14-MAR-2000; 2000US-0189167.
PR   24-MAR-2000; 2000US-0192099.
PR   29-MAR-2000; 2000US-0193480.
PR   15-MAY-2000; 2000US-0205230.
PR   09-JUN-2000; 2000US-0211315.
PR   25-JUL-2000; 2000US-0220534.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS   Claim 1; Page 1361; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity.
XX
SQ   Sequence 514 BP; 113 A; 141 C; 130 G; 126 T; 4 other;

Alignment Scores:
Pred. No.:              1.12e-81        Length:         514
Score:                  90.00           Matches:        90
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            25.71%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-37 (1-350) x AAL15105 (1-514)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 181

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 241

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 301

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 361

Qy         81 TrpLysGluArgLeuValIleArgAlaLeu 90
              ||||||||||||||||||||||||||||||
Db        362 TGGAAGGAGCGCCTGGTGATCCGGGCTCTG 391

RESULT 14
ABA46423/c
ID   ABA46423 standard; DNA; 465 BP.
XX
AC   ABA46423;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human breast cell single exon nucleic acid probe #5118.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00662.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes -
XX
PS   Claim 1; SEQ ID NO 5118; 327pp + sequence listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a single exon nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 465 BP; 138 A; 109 C; 93 G; 125 T; 0 other;
```

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Alignment Scores:
Pred. No.:              1.83e-64        Length:         465
Score:                  73.00           Matches:        73
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            20.86%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-37 (1-350) x ABA46423 (1-465)

Qy       47 ThrGluGluValMetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHis 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      463 ACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCAT 404

Qy       67 ProProIlePheArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuVal 86
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      403 CCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTG 344

Qy       87 IleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAla 106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      343 ATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCG 284

Qy      107 ProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 119
           |||||||||||||||||||||||||||||||||||||||
Db      283 CCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGT 245

RESULT 15
ABA57019/c
ID   ABA57019 standard; DNA; 465 BP.
XX
AC   ABA57019;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #5324.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 1; SEQ ID NO 5324; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 465 BP; 138 A; 109 C; 93 G; 125 T; 0 other;

Alignment Scores:
Pred. No.:              1.83e-64        Length:         465
Score:                  73.00           Matches:        73
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            20.86%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-37 (1-350) x ABA57019 (1-465)

Qy       47 ThrGluGluValMetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHis 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      463 ACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCAT 404

Qy       67 ProProIlePheArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuVal 86
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      403 CCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTG 344

Qy       87 IleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAla 106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      343 ATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCG 284

Qy      107 ProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 119
           |||||||||||||||||||||||||||||||||||||||
Db      283 CCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGT 245


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Job time : 269 secs
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